

Fig. 2

Fig. 3(A)

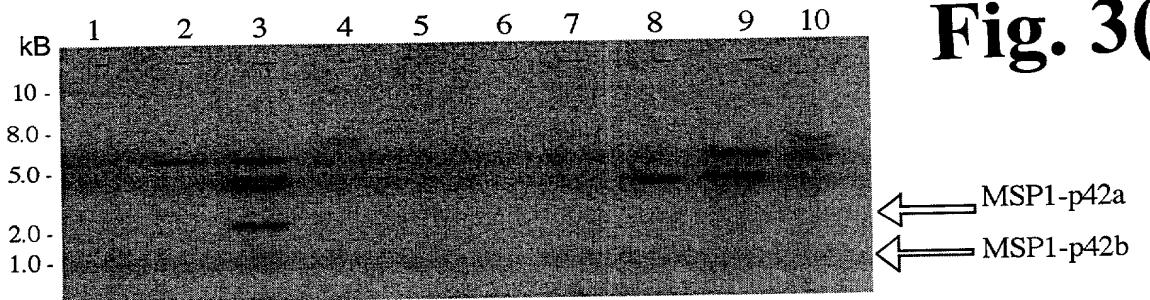


Fig. 3(B)

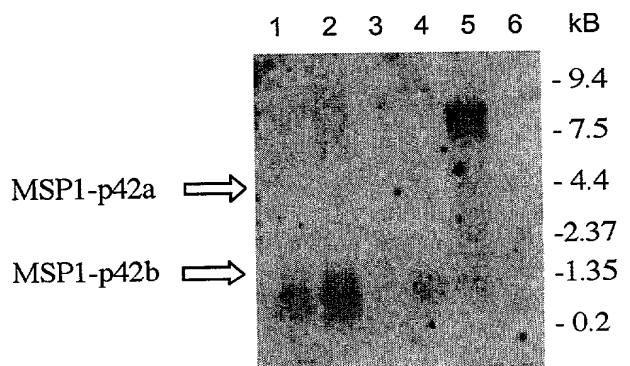


Fig. 4(A)

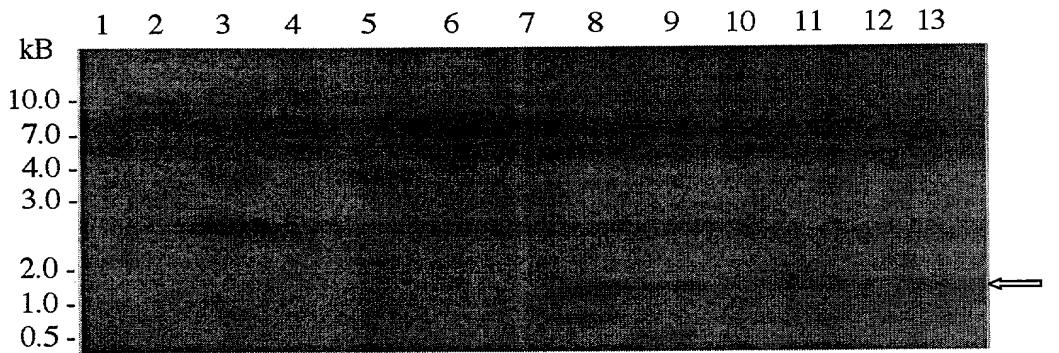
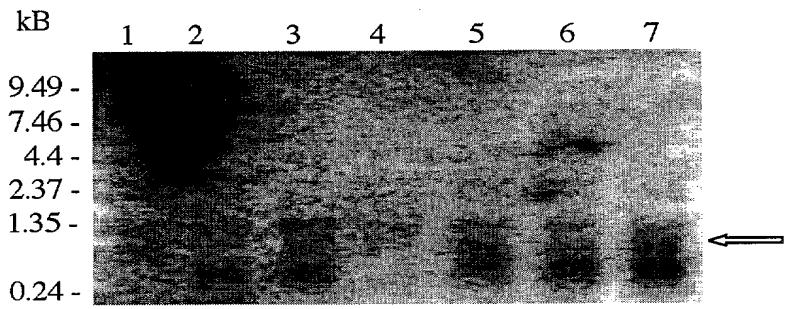


Fig. 4(B)



Wt Std 1 2 3 6 7 8 10 11 12 16 17 18

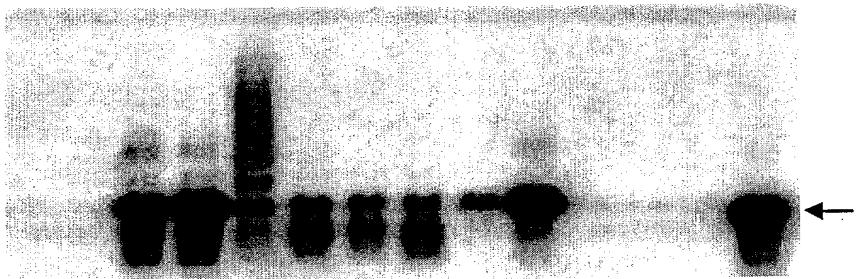


Fig. 5(A)

Wt 1 2 3 4 5 6 7 8 9 10 11 12

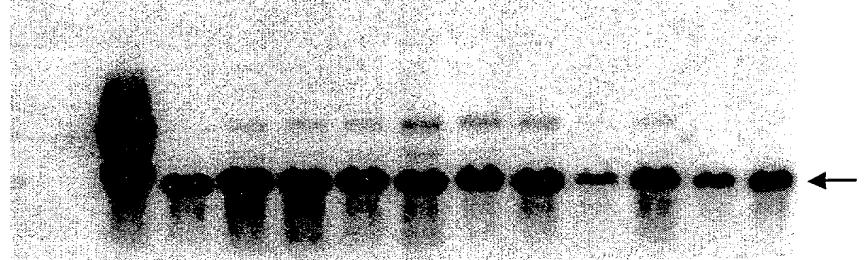


Fig. 5(B)

Fig. 6(A)

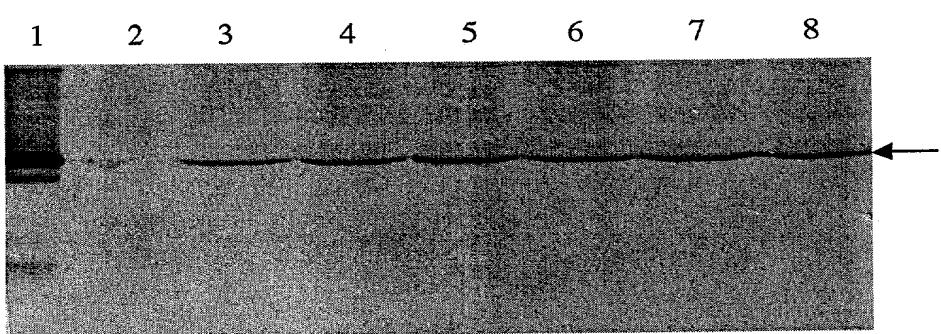
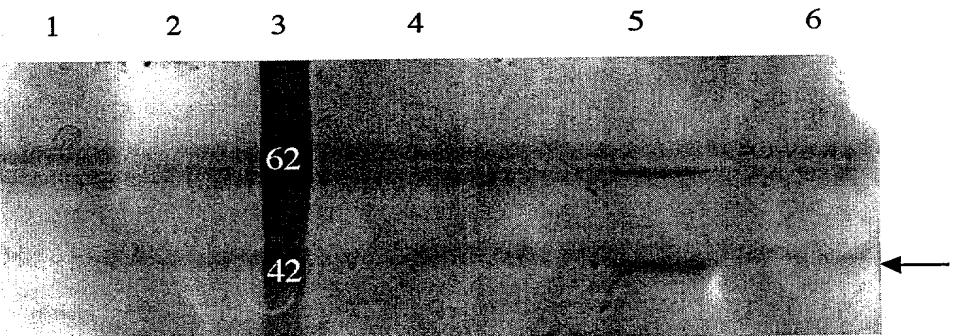


Fig. 6(B)

Fig. 7(A)

MSP1.p42 FUP

401 AAAATGATATTAAAT TTGCACAGGA AGGTATAAG TTATTATGAAAAGGTT
601 AACATTGAGAC CTTATACAATAAC TTAGTTAATAAAAT TGACGATTACTT
951 TCCAGAAAAT TCTGGATGTTCAGAC ATTTAGATGAAAG AGAAGAATGTA

MSP1.p42FVO

181 AATTCAAAATG TTTAGAACAGATTTA ATTCCATATAAAG ATTTA
230 ACATCAAGTAATT ATGTTGTCAAAGATCCA TATAAATTCTTAATAAA
277 GAAAAAAGAGA TAAATTCTTAAGCAGTTA TAATTATATTAAGGATTC

Fig. 7(B)

20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480 500 520 540 560 580 600 620 640 660 680 700 720 740 760 780 800 820 840 860 880 900 920 940 960 980 1000

A E F D N I L S D N I L S G F E N E	18
GCC GAA TTC GAC AAC ATC CTC AGT GAC AAC ATC CTC AGT GGC TTC GAG AAC GAG	54
Y D V I Y L K P L A G V Y R S L K K	36
TAC GAC GTA ATC TAC CTA AAG CCC CTT GCC GGT GTC TAC CGT TCA TTG AAG AAA	108
Q I E K N I F T F N L N L N D I L N	54
CAG ATA GAA AAG AAT ATT TTC ACG TTC AAC CTC AAC CTA AAT GAC ATC CTC AAC	162
S R L K K R K Y F L D V L E S D L M	72
TCG CGC CTC AAG AAG CGA AAA TAC TTC CTC GAC GTG TTG GAA TCC GAC CTT ATG	216
Q F K H I S S N E Y I I E D S F K L	90
CAA TTC AAG CAC ATT AGC TCT AAC GAG TAC ATC ATA GAG GAC AGC TTC AAG CTC	270
L N S E Q K N T L L K S Y K Y I K E	108
TTG AAT TCA GAA CAG AAG AAC ACC CTC CTA AAG TCC TAC AAA TAC ATT AAG GAG	324
S V E N D I K F A Q E G I S Y Y E K	126
TCT GTT GAG AAC GAC ATC AAG TTC GCC CAG GAA GGA ATT AGC TAC TAT GAG AAA	378
V L A K Y K D D L E S I K K V I K E	144
GTC CTG GCT AAA TAC AAG GAC GAC TTG GAA AGC ATT AAG AAG GTA ATC AAA GAA	432
E K E K F P S S P P T T P P S P A K	162
GAG AAG GAA AAG TTT CCG AGC TCT CCA CCC ACA ACT CCC CCA TCG CCT GCA AAG	486
T D E Q K K E S K F L P F L T N I E	180
ACC GAC GAG CAG AAA AAA GAA AGT AAG TTC CTT CCA TTC CTC ACC AAC ATC GAA	540
T L Y N N L V N K I D D Y L I N L K	198
ACT CTA TAT AAC AAC CTG GTG AAC AAG ATT GAT GAC TAC TTA ATC AAC TTG AAG	594
A K I N D C N V E K D E A H V K I T	216
GCG AAA ATT AAT GAC TGT AAC GTC GAA AAG GAT GAA GCC CAC GTT AAG ATC ACC	648
K L S D L K A I D D K I D L F K N H	234
AAG CTT TCC GAT CTC AAA GCC ATC GAC GAT AAG ATT GAC CTG TTT AAG AAC CAC	702
N D F D A I K K L I N D D T K K D M	252
AAC GAT TTC GAC GCA ATC AAA AAG TTG ATC AAC GAC GAT ACT AAG AAA GAC ATG	756
L G K L L S T G L V Q N F P N T I I	270
CTT GGA AAA CTG CTG TCG ACA GGC TTG GTC CAA AAC TTC CCG AAC ACC ATT ATA	810
S K L I E G K F Q D M L N I S Q H Q	288
AGC AAG CTG ATC GAA GGA AAG TTT CAG GAT ATG CTG AAC ATC TCT CAG CAT CAA	864
C V K K Q C P E N S G C F R H L D E	306
TGC GTG AAG AAG CAA TGT CCC GAG AAT TCA GGT TGC TTC CGC CAC TTA GAC GAA	918
R E E C K C L L N Y K Q E G D K C V	324
AGG GAG GAA TGT AAA TGC CTG CTG AAT TAT AAA CAG GAA GGA GAC AAG TGC GTA	972
E N P N P T C N E N N G G C D A D A	342
GAG AAT CCT AAC CCA ACC TGT AAC GAA AAT AAC GGT GGC TGC GAT GCT GAC GCT	1026
K C T E E D S G S N G K K I T C E C	360
AAG TGT ACC GAG GAG GAC AGC GGT TCC AAT GGC AAG AAA ATA ACT TGC GAA TGC	1080
T K P D S Y P L F D G I F C S H D E	378
ACG AAG CCC GAT AGT TAC CCT CTC TTC GAC GGT ATC TTC TGC TCC CAT GAT GAG	1134
L * E L T	383
CTT TAA GAG CTC ACC	

Fig. 8

R	I	Q	G	D	I	T	M	D	N	I	L	S	G	F	E	N	E	18
CGG	ATC	CAA	GGG	GAT	ATA	ACA	ATG	GAC	AAC	ATC	CTC	AGT	GGC	TTC	GAG	AAC	GAG	54
Y	D	V	I	Y	L	K	P	L	A	G	V	Y	R	S	L	K	K	36
TAC	GAC	GTA	ATC	TAC	CTA	AAG	CCC	CTT	GCC	GGT	GTC	TAC	CGT	TCA	TTG	AAG	AAA	108
Q	I	E	K	N	I	F	T	F	N	L	N	L	N	D	I	L	N	54
CAG	ATA	GAA	AAG	AAT	ATT	TTC	ACG	TTC	AAC	CTC	AAC	CTA	AAT	GAC	ATC	CTC	AAC	162
S	R	L	K	K	R	K	Y	F	L	D	V	L	E	S	D	L	M	72
TCG	CGC	CTC	AAG	AAG	CGA	AAA	TAC	TTC	CTC	GAC	GTG	TTG	GAA	TCC	GAC	CTT	ATG	216
Q	F	K	H	I	S	S	N	E	Y	I	I	E	D	S	F	K	L	90
CAA	TTC	AAG	CAC	ATT	AGC	TCT	AAC	GAG	TAC	ATC	ATA	GAG	GAC	AGC	TTC	AAG	CTC	270
L	N	S	E	Q	K	N	T	L	L	K	S	Y	K	Y	I	K	E	108
TTG	AAT	TCA	GAA	CAG	AAG	ACC	CTC	CTA	AAG	TCC	TAC	AAA	TAC	ATT	AAG	GAG		324
S	V	E	N	D	I	K	F	A	Q	E	G	I	S	Y	Y	E	K	126
TCT	GTT	GAG	AAC	GAC	ATC	AAG	TTC	GCC	CAG	GAA	GGG	ATT	AGC	TAC	TAT	GAG	AAA	378
V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	144
GTC	CTG	GCT	AAA	TAC	AAG	GAC	GAC	TTG	GAA	AGC	ATT	AAG	AAG	GTA	ATC	AAA	GAA	432
E	K	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	162
GAG	AAG	GAA	AAG	TTT	CCG	AGC	TCT	CCA	CCC	ACA	ACT	CCC	CCA	TCG	CCT	GCA	AAG	486
T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	180
ACC	GAC	GAG	CAG	AAA	AAA	GAA	AGT	AAG	TTC	CTT	CCA	TTC	CTC	ACC	AAC	ATC	GAA	540
T	L	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	198
ACT	CTA	TAT	AAC	AAC	CTG	GTG	AAC	AAG	ATT	GAT	GAC	TAC	TTA	ATC	AAC	TTG	AAG	594
A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	216
GCG	AAA	ATT	AAT	GAC	TGT	AAC	GTC	GAA	AAG	GAT	GAA	GCC	CAC	GTT	AAG	ATC	ACC	648
K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	234
AAG	CTT	TCC	GAT	CTC	AAA	GCC	ATC	GAC	GAT	AAG	ATT	GAC	CTG	TTT	AAG	AAC	CAC	702
N	D	F	D	A	I	K	K	L	I	N	D	D	T	K	K	D	M	252
AAC	GAT	TTC	GAC	GCA	ATC	AAA	AAG	TTG	ATC	AAC	GAC	GAT	ACT	AAG	AAA	GAC	ATG	756
L	G	K	L	L	S	T	G	L	V	Q	N	F	P	N	T	I	I	270
CTT	GGA	AAA	CTG	CTG	TCG	ACA	GGC	TTG	GTC	CAA	AAC	TTC	CCG	AAC	ACC	ATT	ATA	810
S	K	L	I	E	G	K	F	Q	D	M	L	N	I	S	Q	H	Q	288
AGC	AAG	CTG	ATC	GAA	GGG	AAG	TTT	CAG	GAT	ATG	CTG	AAC	ATC	TCT	CAG	CAT	CAA	864
C	V	K	K	Q	C	P	E	N	S	G	C	F	R	H	L	D	E	306
TGC	GTG	AAG	AAG	CAA	TGT	CCC	GAG	AAT	TCA	GGT	TGC	TTC	CGC	CAC	TTA	GAC	GAA	918
R	E	E	C	K	C	L	L	N	Y	K	Q	E	G	D	K	C	V	324
AGG	GAG	GAA	TGT	AAA	TGC	CTG	CTG	AAT	TAT	AAA	CAG	GAA	GGA	GAC	AAG	TGC	GTA	972
E	N	P	N	P	T	C	N	E	N	N	G	G	C	D	A	D	A	342
GAG	AAT	CCT	AAC	CCA	ACC	TGT	AAA	AAC	GAA	AAT	AAC	GGT	GGC	TGC	GAT	GCT	GAC	1026
K	C	T	E	E	D	S	G	S	N	G	K	K	I	T	C	E	C	360
AAG	TGT	ACC	GAG	GAG	GAC	GGT	TCC	AAT	GGC	AAG	AAA	ATA	ACT	TGC	GAA	TGC		1080
T	K	P	D	S	Y	P	L	F	D	G	I	F	C	S	H	D	E	378
ACG	AAG	CCC	GAT	AGT	TAC	CCT	CTC	TTC	GAC	GGT	ATC	TTC	TGC	TCC	CAT	GAT	GAG	1134
L	*	E	L	T														383
CTT	TAA	GAG	CTC	ACC														1149

Fig. 9

Fig. 10

DNA AND AMINO ACID SEQUENCE OF BVP42-M

attggatccactaaa

13 atgtggtcttggaaagtgtctttattctggcgtctgggtgacc
M W S W K C L L F W A V L V T
58 gccactcttgcacagcagcgatctgttactatggacaacatc
A T L C T A A I S V T M D N I
103 ctcagtggttcgagaacgagtaacgacgtaatctaccaaagccc
L S G F E N E Y D V I Y L K P
148 cttgccggtgtctaccgttcatggaaagaaacagatagaaaagaat
L A G V Y R S L K K Q I E K N
193 atttcacgttcaacctcaacctaataatgacatcctcaactcgcc
I F T F N L N L N D I L N S R
238 ctcaagaagcgaaaatacttcctcgacgtgttggaatccgacctt
L K K R K Y F L D V L E S D L
283 atgcaatttaagcacattagctctaacgagtacatcatagaggac
M Q F K H I S S N E Y I I E D
328 agcttcaagctttgaattcagaacagaacaccctcctaaag
S F K L L N S E Q K N T L L K
373 tcctacaaatacattaaggagtctgttggaaacatcaagttc
S Y K Y I K E S V E N D I K F
418 gcccaggaaggaatttagctactatgagaaagtccctggctaaatac
A Q E G I S Y Y E K V L A K Y
463 aaggacgacttggaaagcattaagaaggtaatcaaagaagagaag
K D D L E S I K K V I K E E K
508 gaaaagttccgagctctccacccacaactccccatcgccctgca
E K F P S S P P T T P P S P A
553 aagaccgacgagcagaaaaaaaagaagtaagttcccttcattcctc
K T D E Q K K E S K F L P F L
598 accaacatcgaaactcttatataacaacctggtaacaagattgat
T N I E T L Y N N L V N K I D
643 gactacttaatcaacttgaaggcgaaaattaatgactgtaacgtc
D Y L I N L K A K I N D C N V
688 gaaaaggatgaagcccacgttaagatcaccaagcttccgatctc
E K D E A H V K I T K L S D L
733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat
K A I D D K I D L F K N H N D
778 ttgcacgcaatcaaaaagttgatcaacgacgataactaagaaagac
F D A I K K L I N D D T K K D
823 atgcttggaaaactgctgtcgacaggcttggtccaaaactcccg
M L G K L L S T G L V Q N F P
868 aacaccattataagcaagctgatcgaagggaaagttcaggatatg

N T I I S K L I E G K F Q D M
913 ctgaacatctctcagcatcaatgcgtgaagaagcaatgtcccgag
L N I S Q H Q C V K K Q C P E
958 aattcaggttgcctccgcacttagacgaaaggaggaatgtaaa
N S G C F R H L D E R E E C K
1003 tgcctgctgaattataaacaggaaggagacaagtgcgtagagaat
C L L N Y K Q E G D K C V E N
1048 cctaaccacccaaacctgtaacgaaaataacggggctgcgatgctgac
P N P T C N E N N G G C D A D
1093 gctaagtgtaccgaggaggacagcggttccaatggcaagaaaata
A K C T E E D S G S N G K K I
1138 acttgcgaatgcacgaagcccatagttaccctcttcgacgg
T C E C T K P D S Y P L F D G
1183 atcttctgctcc
I F C S

ccacccatcatcatcatcatcattaataaggtaaccta
P P H H H H H * *